IN THE CLAIMS

Please amend the claims as follows:

Claims 1-23 (Cancelled)

Claim 24 (Currently Amended): A method for determining whether a cell carries a gene encoding an ABCG2 transporter protein with ~~predicting if a human cell has~~ a decreased capacity to excrete compound B comprising:

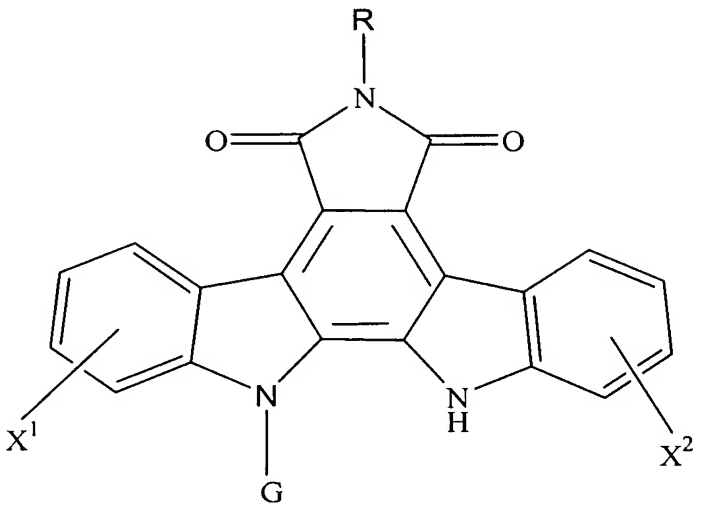
performing an assay on a biological sample from a human cell and determining the nucleotide present at position 421 of SEQ ID NO: 1, wherein the presence of the nucleotide A at position 421 indicates that the cell carries a gene encoding an ABCG2 transporter protein having a decreased capacity to excrete compound B compared to a gene having the nucleotide C at position 421 of SEQ ID NO: 1

~~collecting a biological sample from a human cell,~~

~~testing the biological sample from said human cell for the presence of the genomic polynucleotide polymorphism of the ABCG2 gene in which C421A polymorphism occurs at nucleotide position 421 of SEQ ID NO: 1,~~

~~wherein the presence of said genomic polynucleotide polymorphism is indicative of a decreased capacity by said cell to excrete compound B~~;

wherein compound B is a compound of formula (I):



(I),

wherein X^1 is 2-hydroxyl group,

X^2 is 10-hydroxyl group,

R is (1-hydroxymethyl-2-hydroxyl) ethylamino group, and

G is a beta-D-glucopyranosyl group.

Claims 25-28 (Cancelled)

Claim 29 (Currently Amended): The method of Claim 24, wherein the ~~human cell~~ biological sample is derived from a patient suffering from cancer.

Claim 30 (Currently Amended): The method of Claim 24, comprising collecting ~~a cell~~ the biological sample from body fluid, skin, root of hair, mucous membrane, internal organs, placenta, or cord blood of a subject prior to performing said assay ~~said testing step~~.

Claim 31 (Currently Amended): The method of Claim 24, ~~which comprises detecting said genomic polynucleotide polymorphism by~~ wherein said assay comprises a direct sequencing method.

Claim 32 (Currently Amended): The method of Claim 24, ~~which comprises detecting said genomic polynucleotide polymorphism by~~ wherein said assay comprises a Taqman method.

Claim 33 (Currently Amended): The method of Claim 24, ~~which comprises detecting said genomic polynucleotide polymorphism by~~ wherein said assay comprises an invader method.

Claim 34 (Currently Amended): The method of Claim 24, ~~which comprises detecting said genomic polynucleotide polymorphism by~~ wherein said assay comprises a mass spectrometric method, an RCA method, or a DNA chip method.

Claim 35-38 (Cancelled)

Claim 39 (Currently Amended): The method of Claim 24, further comprising testing whether said human cell has at least one other genomic polynucleotide polymorphism at a nucleotide other than position 421 of SEQ ID NO: 1.

Claim 40 (Previously Presented): The method of Claim 39, wherein said at least one other genomic polynucleotide polymorphism occurs at nucleotide position 34 of SEQ ID NO: 1.

Claim 41 (Previously Presented): The method of Claim 39, wherein said at least one other genomic polynucleotide polymorphism occurs at nucleotide position 376 of SEQ ID NO: 1.

Claim 42 (Previously Presented): The method of Claim 39, wherein said at least one other genomic polynucleotide polymorphism causes amino acid substitution at position 12 of SEQ ID NO: 2.

Claim 43 (Previously Presented): The method of Claim 39, wherein said at least one other genomic polynucleotide polymorphism causes amino acid termination at position 126 of SEQ ID NO: 2.

Claims 44-46 (Not Entered, Cancelled)

Claim 47 (Currently Amended): The method of Claim 24, wherein said assay comprises: ~~polymorphism is detected by a method using a fluorescent energy transfer phenomenon where hybridization of an allele-specific oligonucleotide to a template is performed simultaneously with PCR, comprising~~:

hybridizing an allele-specific probe which is labeled with a fluorescent dye and a quencher to a target site, simultaneously amplifying the region including the site whereupon the hybridization probe is cleaved by 5'-nuclease activity of Taq polymerase as the elongation reaction from the primer proceeds with PCR and detecting exponentially potentiated fluorescence of fluorescent dye which is separated from the quencher.

Claim 48 (Currently Amended): The method of Claim 24, wherein said assay comprises:

~~polymorphism is detected by a method comprising:~~

hybridizing a first probe which is substantially complementary to a first site of the target nucleotide sequence, hybridizing a second probe to a second site of the target nucleotide sequence where the second probe is complementary to its 3'-terminal side and a sequence called a flap which is non-complementary to the template to form a single strand in its 5-terminal side, invading hybridization of the second probe with the target nucleotide sequence at an SNP site by the 3-terminal of the first probe, liberating the flap from the second probe by cleavase, binding of the flap to a FRET probe which includes a sequence complementary to the flap and self-complementary sequence being labeled with both a fluorescent dye and a quencher, cleaving the part of the fluorescent dye in the FRET probe by cleavase, quantifying fluorescence of the cleaved fluorescent dye.